Bioconductor LaTeX Style 2.0

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July 21, 2017

Abstract

This vignette describes the new Bioconductor LaTeX document style. It aims to be at once a demonstration of the features of the style and a guide to their use. The vignette focuses on the use with documents typeset as markup .Rnw files and processed using *Sweave*[1] or *knitr*[2]. The same style is also applied to *R* markdown .Rmd files which are rendered to PDF output format.

Package

BiocStyle 2.4.1

Report issues on https://github.com/Bioconductor/BiocStyle/issues

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1 Authoring package vignettes

1.1 Getting started

BiocStyle provides standard formatting of documents rendered to PDF output format. It consists of a LATEX document style definition which can be used with either plain *Sweave*, *knitr*, or *rmarkdown*. To enable *BiocStyle* in your package vignette follow the instructions below depending on the input format.

1.1.1 *Sweave*

To use with *Sweave*, add the following to your package 'DESCRIPTION' file:

```
Suggests: BiocStyle
```

and add this code chunk to the preamble[1] of your .Rnw file:

```
<<style-Sweave, eval=TRUE, echo=FALSE, results=tex>>=
BiocStyle::latex2()
@
```

See `?latex2` for additional options. It is not necessary to include \usepackage{Sweave} in your document preamble, as it is already inserted by *BiocStyle*. See Appendix B for a list of other automatically attached LATEX packages.

[1] before the \begin{document} command, and preferably right after the \documentclass definition

1.1.2 *knitr*

To use with *knitr*, add the following to the 'DESCRIPTION' file:

```
VignetteBuilder: knitr
Suggests: BiocStyle, knitr
```

this to the top of the .Rnw file:

```
%\VignetteEngine{knitr::knitr}
```

and this to the preamble:

```
<<style-knitr, eval=TRUE, echo=FALSE, results="asis">>=
BiocStyle::latex2()
@
```

See `?latex2` for additional options, and Appendix B for a list of automatically attached LATEX packages.

1.1.3 R markdown

To enable *BiocStyle* in your *R* markdown vignette you need to:

1. Edit to the 'DESCRIPTION' file by adding

   ```
   VignetteBuilder: knitr
   Suggests: BiocStyle, knitr, rmarkdown
   ```

2. Specify `BiocStyle::pdf_document2` as the output format and add vignette metadata to the document header:

```
---
title: "Vignette Title"
author: "Vignette Author"
output:
  BiocStyle::pdf_document2
vignette: >
  %\VignetteIndexEntry{Vignette Title}
  %\VignetteEngine{knitr::rmarkdown}
  %\VignetteEncoding{UTF-8}
---
```

The `vignette` section is required in order to instruct *R* how to build the vignette. Note that `\VignetteIndexEntry` should match the `title` of your vignette.

See the *Authoring R Markdown vignettes* package vignette for more details on authoring markdown documents with *BiocStyle*.

1.2   Workflow

Provided that *BiocStyle* has been installed, a convenient way to build the vignette as it is being written is with the command

```
R CMD Sweave --pdf vignette.Rnw
```

A short-cut useful for checking the LATEX portion of vignettes is to toggle evaluation of code chunks to `FALSE`.

```
SWEAVE_OPTIONS="eval=FALSE" R CMD Sweave --pdf vignette.Rnw
```

When using *knitr*, the command to process the vignette is

```
R CMD Sweave --engine=knitr::knitr --pdf vignette.Rnw
```

For *R* markdown vignettes, set the engine to `knitr::rmarkdown`.

```
R CMD Sweave --engine=knitr::rmarkdown --pdf vignette.Rmd
```

By default, *knitr* automatically caches results of vignette chunks, greatly accelerating the turnaround time required for edits. Both the default and *knitr* incantations create PDF files using `texi2dvi --pdf`; many versions of this software incorrectly display non-breaking spaces as a tilde, ~. This can be remedied (as on the *Bioconductor* build system) with a final run of

```
R CMD texi2dvi --pdf vignette.tex
R CMD pdflatex vignette.tex
```

2   Structuring the document

2.1   Title page

Important: most of the methods described here only work once BiocStyle is loaded; therefore, specify title and authors after *the code chunk calling* `BiocStyle::latex2()`.

2.1.1   Title and running headers

Create a title and running headers by defining \bioctitle and \author in the preamble

```
\bioctitle[Short title for headers]{Full title for title page}
%% also: \bioctitle{Title used for both header and title page}
%% or... \title{Title used for both header and title page}
\author{Vignette Author\thanks{\email{user@domain.com}}}
```

and use \maketitle at the beginning of the document to output the title and author information.

2.1.2   Authors and affiliations

As illustrated above, use the \email command to enter hyperlinked email addresses typeset in monospace font. Multiple author affiliations can be specified with the help of the LaTeX package authblk which is automatically loaded by *BiocStyle*. See the following examples for typical use cases.

If your vignette has just a single author, use standard LaTeX syntax to enter the author and affiliation information separated by a new line. You can provide the email address in \thanks, or in another new line after the affiliation.

```
\author{Vignette Author\thanks{\email{user@domain.com}}\\
        Author's Affiliation}
```

In case of multiple authors, you can specify the author and affiliation information in different manners depending on the number of affiliations. In the basic case, when you don't provide authors' affiliation, or all the authors share the same affiliation, you can just use the regular \author command:

```
\author{
  First Author\thanks{\email{first@author.com}},
  Second Author\thanks{\email{second@author.com}}\\
  Shared Affiliation
}
```

To provide different affiliations, some of which are potentially shared, enter each author separately and use \affil to specify affiliation. The authors will appear all in one (possibly continued) line with automatic footnotes, and the affiliations are displayed in separate lines below.[2]

[2]as on this vignette's title page

```
\author{First Author}
\author{Second Author}
\affil{First and Second authors' shared affiliation}
\author{Third Author\thanks{\email{corresponding@author.com}}}
```

```
\affil{Third author's affiliation}
```

In the case when some authors have more than one affiliation, or the authors with a shared affiliation do not come one after another, you need to manually define footnote markers as optional arguments to \author and \affil commands, as in the following example.

```
\author[1,2]{First Author\thanks{\email{user@domain.com}}}
\author[1]{Second Author}
\author[2]{Third Author}
\affil[1]{First and Second authors' affiliation}
\affil[2]{First and Third authors' affiliation}
```

2.1.3 Abstract, package version, and table of contents

Abstract can be entered using the standard `abstract` environment:

```
\begin{abstract}
   Short summary of the vignette's content.
\end{abstract}
```

It is recommended to include information on the specific package version described in the vignette. The following line[3] inserts this information automatically and in a properly formatted manner.

[3]substitute `packageName` by the name of your package

```
\packageVersion{\Sexpr{BiocStyle::pkg_ver("packageName")}}
```

Use \tableofcontents to include a hyperlinked table of contents (TOC), and \section, \subsection, \subsubsection for structuring your document. It is a good practice to start the first section on a new page by calling \newpage after the TOC:

```
\tableofcontents
\newpage
\section{My First Section}
```

2.2   Style macros

BiocStyle introduces the following additional markup styling commands useful in typical *Bioconductor* vignettes.

Software:

- \R{} and \Bioconductor{} to reference *R* software and the *Bioconductor* project.

- \software{GATK} to reference third-party software, e.g., *GATK*.

Packages:

- \Biocpkg{IRanges} for *Bioconductor* software, annotation and experiment data packages, including a link to the release landing page or if the package is only in devel, to the devel landing page. *IRanges*.

- \CRANpkg{data.table} for *R* packages available on CRAN, including a link to the FHCRC CRAN mirror landing page, *data.table*.

- \Githubpkg{rstudio/rmarkdown} for *R* packages available on GitHub, including a link to the package repository, *rmarkdown*.

- \Rpackage{MyPkg} for *R* packages that are *not* available on *Bioconductor* or CRAN, *MyPkg*.

Code:

- \Rfunction{findOverlaps} for functions `findOverlaps`.
- \Robject{olaps} for variables `olaps`.
- \Rclass{GRanges} when referring to a formal class *GRanges*.
- \Rcode{log(x)} for *R* code, `log(x)`.

Communication:

- \bioccomment{additional information for the user} communicates *Comment: additional information for the user*.
- \warning{common pitfalls} signals *Warning: common pitfalls*.
- \fixme{incomplete functionality} provides an indication of *FixMe: incomplete functionality*.

For all of the above message types, the default opening word can be overriden in an optional argument, e.g. \fixme[TODO]{missing functionality} produces *TODO: missing functionality*.

General:

- \email{user@domain.com} to provide a linked email address, user@domain.com.
- \file{script.R} for file names and file paths 'script.R'.

2.3 Code chunks

BiocStyle automatically adjusts the line length[4] of output code chunks depending on the document's font size setting. Therefore, it shouldn't be necessary to set it manually. If for some reason you wish to alter it, use the `width` argument in the call to `BiocStyle::latex2`.

[4]`options("width")`

2.4 Figures

In addition to the standard \figure environment *BiocStyle* provides special environments for small and wide figures. These three environments differ in size, default aspect ratio[5], and horizontal placement on the the page. See the following table for details, and Figures 1, 2 and 3 for examples.

[5]device dimensions are automatically set only by *knitr* and *rmarkdown*, and not by *Sweave*

environment	description	output width	device dimensions	aspect ratio
figure	regular figure	120mm (≈4.72in)	8 × 5 in	1.6
figure*	wide figure	150mm (≈5.90in)	10 × 5 in	2.0
smallfigure	small figure	75mm (≈2.95in)	5 × 5 in	1.0

The `figure` environment produces regular figures which are left-indented and right-aligned with the paragraph, as Figure 1. To utilize the whole available width use the `figure*` environment. It produces figures which are left-aligned with the paragraph and extend on the right margin (Figure 2). The `smallfigure` environment is meant for possibly rectangular plots
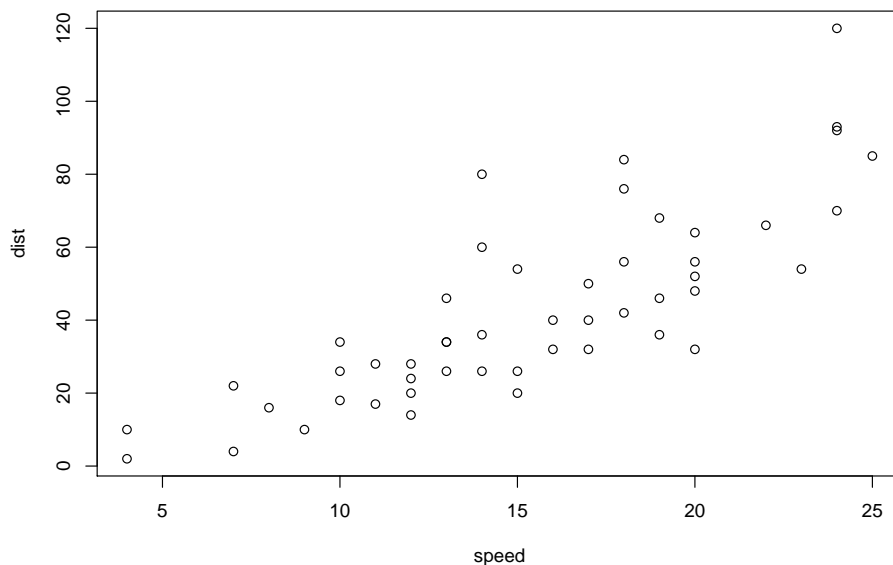
Figure 1: Regular figure
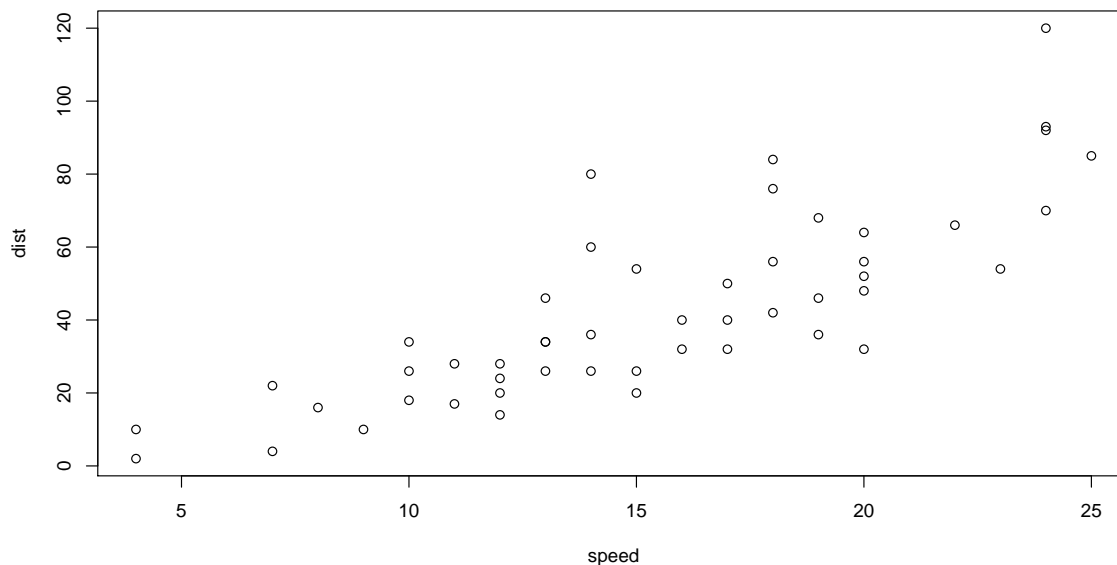A plot displayed with the `\figure` environment.

Figure 2: Wide figure
A plot displayed with the `\figure*` environment.

which are about half as wide as the paragraph (Figure 3). The default placement specifier for *BiocStyle* floats is htbp, which typically outputs them in the place where they are defined. The first sentence of figure captions is emphasized to serve as figure title. This feature can be disabled be setting the argument `titlecaps=FALSE` in the call to `BiocStyle::latex2`.

To use figure environments in *Sweave*, write explicit LaTeX code which inserts them in combination with the *Sweave* option include=FALSE. For example, Figure 2 was produced with the following code.

```
<<widefig, echo=FALSE, fig=TRUE, include=FALSE, width=10, height=5>>=
```
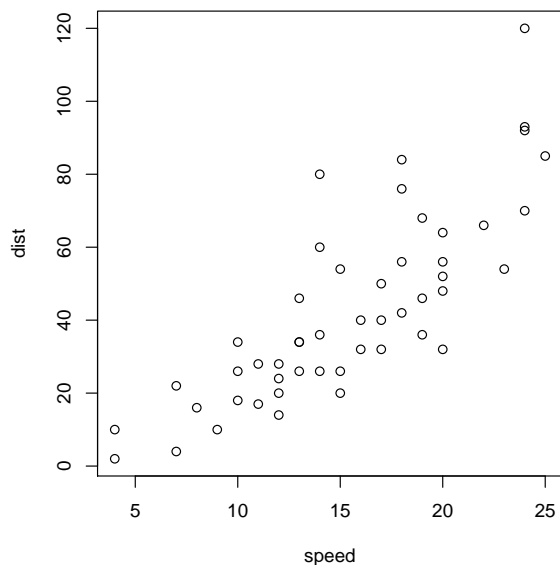
Figure 3: Small figure
A plot displayed with the \smallfigure environment.

```
par(mar=c(4,4,0.5,0.5))
plot(cars)
@

\begin{figure*}
  \includegraphics{\jobname-widefig}
  \caption{\label{fig:wide}Wide figure. A plot displayed
  with the {\ttfamily\textbackslash figure*} environment.}
\end{figure*}
```

In *knitr* and *rmarkdown* the output environment for a graphics-producing code chunk can be specified in `fig.env` chunk option, e.g. set `fig.env='smallfigure'` to get \begin{smallfigure}. It is also possible to specify the wide and small figure environments by setting `fig.wide` or `fig.small` option to `TRUE`. The following two *knitr* code chunks are equivalent and produce the same output, similar to Figure 3.

```
<<smallfig, fig.cap="Small figure.", fig.env="smallfigure">>=
plot(cars)
@

<<smallfig, fig.cap="Small figure.", fig.small=TRUE>>=
plot(cars)
@
```

Specify `fig.width` and/or `fig.height` to override the default device dimensions listed in the table on page 7. To adjust the aspect ratio use `fig.asp`. For example, the following code would produce a full-width square plot, as in Figure 4.

```
<<square, fig.wide=TRUE, fig.asp=1>>=
plot(cars)
@
```
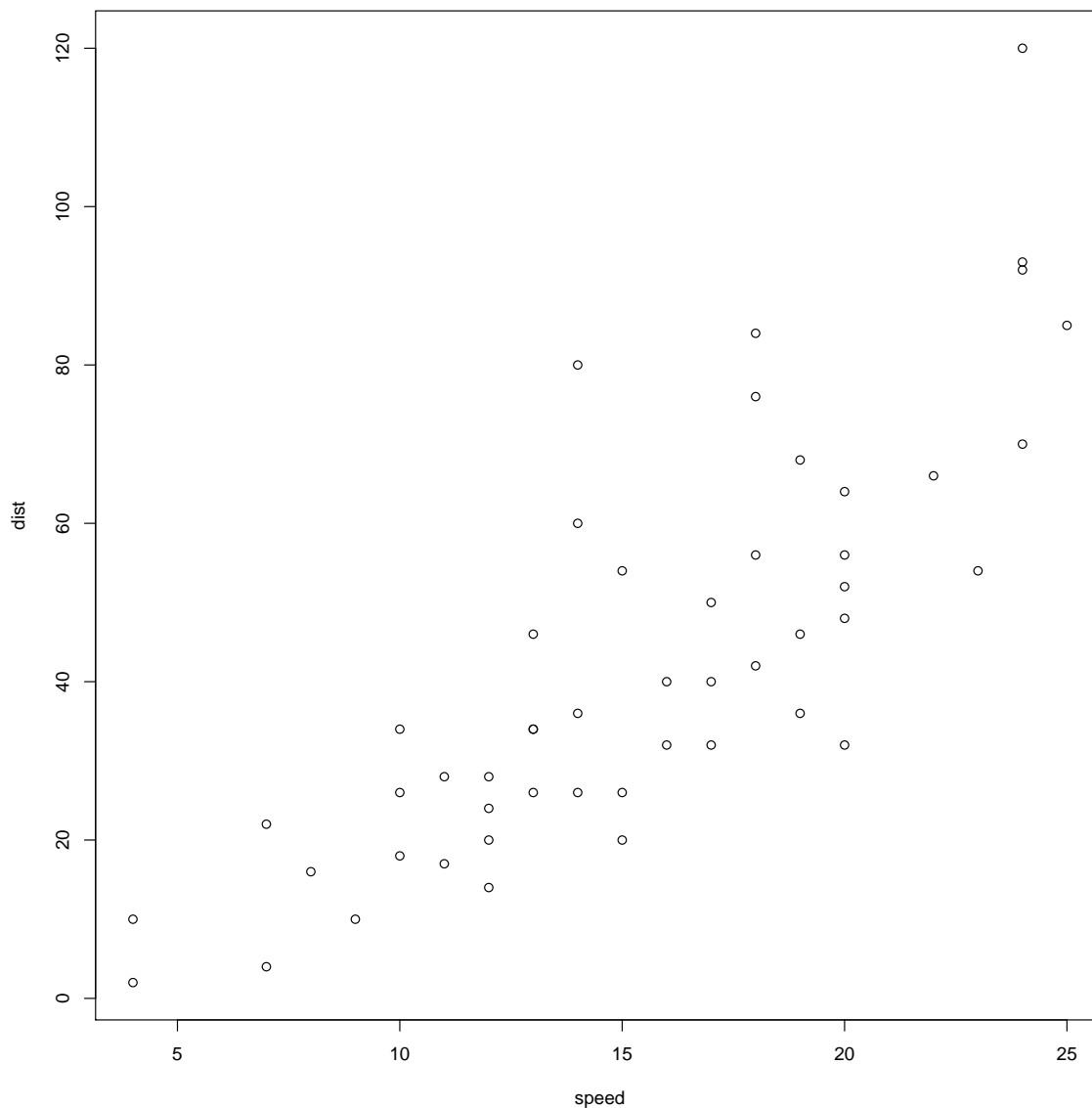
Figure 4: Full-width square figure
Use `fig.wide=TRUE, fig.asp=1` code chunk options to enter with *knitr* or *rmarkdown*.

When *knitr* is used plots are cropped so that blank margins around them are removed to make better use of the space in the output document[6]. This feature can be switched off by setting the chunk option `knitr::opts_chunk$set(crop = NULL)`.

[6]otherwise one often has to struggle with `par` to set appropriate margins

2.4.1 `\incfig` convenience macro

Besides the usual LATEX capabilities (the `figure` environment and `\includegraphics` command) *BiocStyle* defines a macro

`\incfig[placement]{filename}{width}{title}{caption}`

which expects four arguments:

filename The name of the figure file, also used as the label by which the float can be referred to by \ref{}. Some *Sweave* and *knitr* options place figures in a subdirectory; unless `short.fignames=TRUE` is set the full file name, including the subdirectory and any prefixes, should be provided. By default, these are '<sweavename>-' for *Sweave* and 'figure/' for *knitr*. Also note the different naming scheme used by *knitr*: figure files are named '<chunkname>-i' where *i* is the number of the plot generated in the chunk.

width Figure width.

title A short title, used in the list of figures and printed in bold as the first part of the caption.

caption Extended description of the figure.

The optional **placement** specifier controls where the figure is placed on page; it takes the usual values allowed by LATEX floats, i.e., a list containing t, b, p, or h, where letters enumerate permitted placements[7].

[7]if no placement specifier is given, the default htbp is assumed

For incfig with *Sweave* use

```
<<figureexample, fig=TRUE, include=FALSE, width=4.2, height=4.6>>=
par(mar=c(4,4,0.5,0.5))
v = seq(0, 60i, length=1000)
plot(abs(v)*exp(v), type="l", col="Royalblue")
@
\incfig{\jobname-figureexample}{0.5\textwidth}{A curve.}
  {The code that creates this figure is shown in the code chunk.}
as shown in Figure~\ref{\jobname-figureexample}.
```

This results in

```
> par(mar=c(4,4,0.5,0.5))
> v = seq(0, 60i, length=1000)
> plot(abs(v)*exp(v), type="l", col="Royalblue")
```
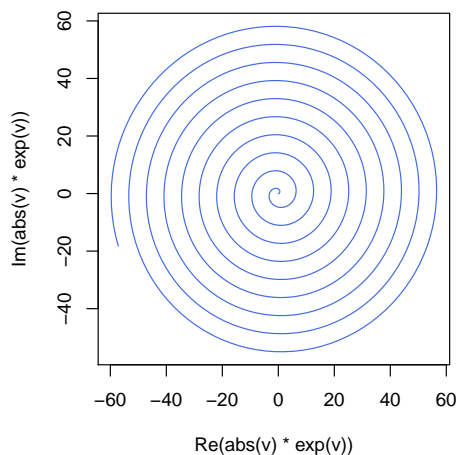

Figure 5: A curve
The code that creates this figure is shown in the code chunk.

as shown in Figure 5.

When option `short.fignames=TRUE` is set, figure names used by `\incfig` and `\ref` do not contain any prefix and are identical to the corresponding code chunk labels (plus figure number in case of *knitr*). For example, in *Sweave* the respective code for the above example would be `\incfig{figureexample}{...}{...}{...}` and `\ref{figureexample}`.

For `\incfig` with *knitr*, use the option `fig.show='hide'` rather than `include=FALSE`. The *knitr*-equivalent code for Figure 5 is:

```
<<figureexample, fig.show='hide', fig.width=4, fig.height=4>>=
par(mar=c(4,4,0.5,0.5))
v = seq(0, 60i, length=1000)
plot(abs(v)*exp(v), type="l", col="Royalblue")
@
```

Note the difference in option names setting the figure width and height compared to *Sweave*. Unless `short.fignames=TRUE` is set, use the default 'figure/' prefix when inserting and referring to figures, e.g.:

```
\incfig{figure/figureexample-1}{0.5\textwidth}{A curve.}
    {The code that creates this figure is shown in the code chunk.}
```

A custom prefix for figure file names can be passed to `latex2` in the `fig.path` argument. When `short.fignames=TRUE`, figures can be referred to directly by code chunk labels, i.e., `\incfig{figureexample-1}...` and `\ref{figureexample-1}`.

2.5 Equations

When referencing equations, e.g. **1**, use `\eqref` to ensure proper label formatting.

$$\sin^2 \theta + \cos^2 \theta \equiv 1 \qquad \qquad \boxed{1}$$

2.6 Footnotes

One of the distinctive features of the style is an asymmetric page layout with a wide margin on the right. This provides additional space for ancillary information in side notes. These can be entered in footnotes[8] typeset as margin notes, which has the advantage that the notes appear close to the place where they are defined.

[8]this is a side note entered using the `\footnote` command

2.7 Bibliography

`BiocStyle::latex2` has default argument `use.unsrturl=TRUE` to automatically format bibliographies using *natbib*'s unsrturl style. There is no need to explicitly include *natbib*, and it is an error to use a `\bibliographystyle` command. The *unsrturl.bst* format, e.g., [1, 2], supports hyperlinks to DOI and PubMed IDs but not `\citet` or `\citep`.

To use a bibliography style different from unsrturl, set `use.unsrturl=FALSE` and follow normal LATEX conventions.

References

[1] Friedrich Leisch. *Compstat: Proceedings in Computational Statistics*, chapter Sweave: Dynamic Generation of Statistical Reports Using Literate Data Analysis, pages 575–580. Physica-Verlag HD, Heidelberg, 2002. URL: http://leisch.userweb.mwn.de/Sweave/, doi:10.1007/978-3-642-57489-4_89.

[2] Yihui Xie. knitr: A comprehensive tool for reproducible research in R. In Victoria Stodden, Friedrich Leisch, and Roger D. Peng, editors, *Implementing Reproducible Computational Research*. Chapman and Hall/CRC, 2014. ISBN 978-1466561595. URL: http://www.crcpress.com/product/isbn/9781466561595.

A   Session info

Here is the output of `sessionInfo()` on the system on which this document was compiled:

- R version 3.4.1 (2017-06-30), `x86_64-pc-linux-gnu`

- Locale: `LC_CTYPE=en_US.UTF-8`, `LC_NUMERIC=C`, `LC_TIME=en_US.UTF-8`, `LC_COLLATE=C`, `LC_MONETARY=en_US.UTF-8`, `LC_MESSAGES=en_US.UTF-8`, `LC_PAPER=en_US.UTF-8`, `LC_NAME=C`, `LC_ADDRESS=C`, `LC_TELEPHONE=C`, `LC_MEASUREMENT=en_US.UTF-8`, `LC_IDENTIFICATION=C`

- Running under: `Ubuntu 16.04.2 LTS`

- Matrix products: default

- BLAS: `/home/biocbuild/bbs-3.5-bioc/R/lib/libRblas.so`

- LAPACK: `/home/biocbuild/bbs-3.5-bioc/R/lib/libRlapack.so`

- Base packages: base, datasets, grDevices, graphics, methods, stats, utils

- Other packages: BiocStyle 2.4.1

- Loaded via a namespace (and not attached): Rcpp 0.12.12, backports 1.1.0, bookdown 0.4, compiler 3.4.1, digest 0.6.12, evaluate 0.10.1, highr 0.6, htmltools 0.3.6, knitr 1.16, magrittr 1.5, rmarkdown 1.6, rprojroot 1.2, stringi 1.1.5, stringr 1.2.0, tools 3.4.1, yaml 2.1.14

B   Attached LATEX packages

BiocStyle loads the following LATEX packages:

`authblk`, `beramono`, `caption`, `changepage`, `color`, `enumitem`, `etoolbox`, `fancyhdr`, `fontenc`, `footmisc`, `framed`, `geometry`, `graphicx`, `hyperref`, `ifthen`, `marginfix`, `mathtools`, `nowidow`, `parnotes`, `parskip`, `placeins`, `ragged2e`, `soul`, `titlesec`, `titletoc`, `xstring`.

C   Known issues

C.1   Compatibility with the *xtable R* package

BiocStyle does not support tables produced by the *R* package *xtable* in plain *Sweave* documents. This limitation does not apply to documents compiled with *knitr*. If you would like to use *xtable* in your *BiocStyle*-enabled document, please consider using *knitr*[9] instead of *Sweave*.

[9]see Sections 1.1.2 and 2.4 for details on using BiocStyle with *knitr*